



#8

SEQUENCE LISTING

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RAPSON, Nicholas Timothy
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<120> Antibodies to CD23, derivatives thereof, and their therapeutic uses

<130> 1430-256/PG3433US

<140> US 09/674,716

<141> 2001-01-22

<150> CA 2,328,606

<151> 1999-05-07

<150> PCT/GB99/01434

<151> 1999-05-07

<150> GB 9809839.5

<151> 1998-05-09

<160> 53

A3
<170> PatentIn Ver. 2.1

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ctg att ttt ttt att gtt ctt tta aaa ggg gtc cag agt gaa gtg aag 95
Leu Ile Phe Phe Ile Val Leu Leu Lys Gly Val Gln Ser Glu Val Lys
20 25 30

ctt gag gag tct gga gga ggc ttg gtg caa cct gga gga tcc atg aaa 143
Leu Glu Glu Ser Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys
35 40 45

ctc tcc tgt gta gcc tct gga ttt act ttc agt ggc tac tgg atg tct 191
Leu Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Gly Tyr Trp Met Ser
50 55 60

tgg gtc cgc cag tct cca gag aag ggg ctt gag tgg gtt gct gaa att 239
Trp Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val Ala Glu Ile
65 70 75

aga ttg aaa tct gat aat tat gca aca cat tat gcg gag tct gtg aaa	287
Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu Ser Val Lys	
80 85 90 95	
ggg aag ttc acc atc tca aga gat gat tcc aaa agt cgt ctc tac ctg	335
Gly Lys Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Arg Leu Tyr Leu	
100 105 110	
caa atg aac agc tta aga gct gaa gac agt gga gtt tat tac tgt aca	383
Gln Met Asn Ser Leu Arg Ala Glu Asp Ser Gly Val Tyr Tyr Cys Thr	
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Val Gln Phe Leu Gly Val Leu Met Phe Trp Ile Ser Gly Val Ser Gly	
20 25 30	
gat att gtg ata acc cag gat gaa ctc tcc aat cct gtc act tct gga	143
Asp Ile Val Ile Thr Gln Asp Glu Leu Ser Asn Pro Val Thr Ser Gly	
35 40 45	
gaa tca gtt tcc atc tcc tgc agg tct agt aag agt ctc ctg tat aag	191
Glu Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Tyr Lys	
50 55 60	
gat ggg aag aca tac ttg aat tgg ttt ctg cag aga cca gga caa tct	239
Asp Gly Lys Thr Tyr Leu Asn Trp Phe Leu Gln Arg Pro Gly Gln Ser	
65 70 75	
cct cag ctc ctg atg tat ttg atg tcc acc cgt gca tca gga gtc tca	287
Pro Gln Leu Leu Met Tyr Leu Met Ser Thr Arg Ala Ser Gly Val Ser	
80 85 90 95	
gac cgg ttt agt ggc agt ggg tca ggc aca gat ttc acc ctg gaa atc	335
Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Glu Ile	
100 105 110	
agt aga gtg aag gct gag gat gtg ggt gtg tat tac tgt caa caa ctt	383
Ser Arg Val Lys Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Leu	
115 120 125	

gta gag tat cca ttc acg ttc ggc tcg ggg aca aag ttg gaa ata aaa 431
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130 135 140

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Arg Thr
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Val Lys Gly

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gtg aag ggg 57
Val Lys Gly

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<210> 14
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Val His Ser

<210> 16
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Ala Gln Ala

<210> 17
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<212> DNA
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gag ccg gcc tcc atc tcc tgt cgc tcg agt aag agt ctc ctg tat aag 96
Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Tyr Lys
20 25 30

gat ggg aag aca tac ttg aat tgg tac ctg cag aag cca ggg cag tct 144
Asp Gly Lys Thr Tyr Leu Asn Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

cca cag ctc ctg atc tat ttg atg tcc acc cgg gca tca ggg gtc cct 192
Pro Gln Leu Leu Ile Tyr Leu Met Ser Thr Arg Ala Ser Gly Val Pro
50 55 60

gac agg ttc agt ggc agt gga tca ggc aca gat ttt aca ctg aaa atc 240
Asp Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

agc aga gtg gag gct gag gat gtt ggg gtt tat tac tgt caa cag ctg 288
Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Leu
85 90 95

gta gag tat cca ttc acg ttc ggc caa ggg acc aag gtg gag atc aaa 336
 Val Glu Tyr Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
 100 105 110

 cgt acg gtg gct 348
 Arg Thr Val Ala
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 <210> 18
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 Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr
 20 25 30

 tgg atg tcc tgg gtc cgc cag gct cca ggg aag ggg ctc gag tgg gtt 144
 Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
 35 40 45

 gct gaa att aga ttg aaa tct gat aat tat gca aca cat tat gcg gag 192
 Ala Glu Ile Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu
 50 55 60

 tct gtg aag ggg aaa ttc acc atc tca aga gat gat tca aaa tct aga 240
 Ser Val Lys Gly Lys Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Arg
 65 70 75 80

 ctg tat ctg caa atg aac agc ctg aaa acc gag gac aca gcc gtg tat 288
 Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
 85 90 95

 tac tgt aca gat ttc ata gac tgg ggc cag gga aca cta gtc acc gtc 336
 Tyr Cys Thr Asp Phe Ile Asp Trp Gly Gln Gly Thr Leu Val Thr Val
 100 105 110

 tcc tca gcc tcc acc aag ggc cca tcg gtc ttc ccc ctg gca ccc tcc 384
 Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
 115 120 125

 tcc aag agc acc tct ggg ggc aca gcg gcc ctg ggc tgc ctg gtc aag 432
 Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
 130 135 140

gac tac ttc ccc gaa ccg gtg acg gtg tcg tgg aac tca ggc gcc ctg		480	
Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu			
145	150	155	160
acc agc ggc gtg cac acc ttc ccg gct gtc cta cag tcc tca gga ctc		528	
Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu			
165	170	175	
tac tcc ctc agc agc gtg gtg acc gtg ccc tcc agc agc ttg ggc acc		576	
Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Leu Gly Thr			
180	185	190	
cag acc tac atc tgc aac gtg aat cac aag ccc agc aac acc aag gtg		624	
Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val			
195	200	205	
gac aag aaa gtg gag ccc aaa tct tgt gac aaa act cac aca tgc cca		672	
Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro			
210	215	220	
ccg tgc cca gca cct gaa ctc gcg ggg gca ccg tca gtc ttc ctc ttc		720	
Pro Cys Pro Ala Pro Glu Leu Ala Gly Ala Pro Ser Val Phe Leu Phe			
225	230	235	240
ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc cct gag gtc		768	
Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val			
245	250	255	
aca tgc gtg gtg gac gtg agc cac gaa gac cct gag gtc aag ttc		816	
Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe			
260	265	270	
aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag aca aag ccg		864	
Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro			
275	280	285	
ccg gag gag cag tac aac agc acg tac cgt gtg gtc agc gtc ctc acc		912	
Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr			
290	295	300	
gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag tgc aag gtc		960	
Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val			
305	310	315	320
tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc tcc aaa gcc		1008	
Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala			
325	330	335	
aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc cca tcc cgg		1056	
Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg			
340	345	350	
gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa ggc		1104	
Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly			
355	360	365	

ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag ccg Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro 370 375 380	1152
gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc gac ggc tcc Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser 385 390 395 400	1200
ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag cag Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln 405 410 415	1248
ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac cac Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His 420 425 430	1296
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<212> DNA	

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<210> 23
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<210> 24
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<210> 25
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<223> Description of Artificial Sequence: Oligo

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<210> 26
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<223> Description of Artificial Sequence: Oligo

<400> 26
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<210> 27
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<213> Artificial Sequence

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<223> Description of Artificial Sequence: Oligo

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cagctgttga cagtaataaa cccc 84

<210> 29
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<223> Description of Artificial Sequence: Oligo

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<210> 31
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<223> Description of Artificial Sequence: Oligo

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<210> 33
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<223> Description of Artificial Sequence: Oligo

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<223> Description of Artificial Sequence: Oligo

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<223> Description of Artificial Sequence: Oligo

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<210> 43
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic sequence

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<210> 44
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic sequence

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<210> 45
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Synthetic sequence

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<210> 46
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<212> DNA
<213> Mus musculus

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aacttccctt tcacagactc cgcataatgt gttgcataat tatcagattt caatctaatt 180

tcagcaaccc actcaagccc cttctctgga gactggcgga cccaaagacat ccagtagcca 240
ctgaaaagtaa atccagaggc tacacaggag agtttcatgg atcctccagg ttgcaccaag 300
cctcctccag actcctcaag cttcacttca ctctggaccc cttttaaaag aacaataaaa 360
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<210> 47
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<212> DNA
<213> Mus musculus

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tgtgcctgac ccactgccac taaaccggtc tgagactcct gatgcacggg tggacatcaa 180
atacatcagg agctgaggag attgtcctgg tctctgcaga aaccaattca agtatgtctt 240
cccattctta tacaggagac tcttactaga cctgcaggag atggaaactg attctccaga 300
agtgacagga ttggagagtt catcctgggt tattcacaata tccccactga ctccagagat 360
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<223> Description of Artificial Sequence: Humanised anti-CD23 antibody light chain variable region

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aaaatctgtg cctgatccac tgccactgaa cctgtcaggg acccctgatg cccgggtgga 180
catcaaataag atcaggagct gtggagactg ccctggcttc tgcaggtacc aattcaagta 240
tgtcttccca tccttataaca ggagactctt actcgagcga caggagatgg aggccggctc 300
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<210> 49
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<223> Description of Artificial Sequence: Humanised anti-CD23 antibody heavy chain variable region

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gctgttagagg aagaaggagc cgtcgagtc cagcacggga ggcgtggctc tggtagtttt 180
ctccggctgc ccattgtct cccactccac ggcgtatgtcg ctggataga agcctttgac 240
caggcagggtc aggctgaccc ggttcttggt cagctcatcc cgggatgggg gcagggtgta 300
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<210> 50

<211> 137

<212> PRT

<213> Mus musculus

<400> 50

Ala Leu Gln Leu Leu Ser Thr Gln Asp Leu Thr Met Asp Phe Gly Leu
1 5 10 15

Ile Phe Phe Ile Val Leu Leu Lys Gly Val Gln Ser Glu Val Lys Leu
20 25 30

Glu Glu Ser Gly Gly Leu Val Gln Pro Gly Gly Ser Met Lys Leu
35 40 45

Ser Cys Val Ala Ser Gly Phe Thr Phe Ser Gly Tyr Trp Met Ser Trp
50 55 60

Val Arg Gln Ser Pro Glu Lys Gly Leu Glu Trp Val Ala Glu Ile Arg
65 70 75 80

Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu Ser Val Lys Gly
85 90 95

Lys Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Arg Leu Tyr Leu Gln
100 105 110

Met Asn Ser Leu Arg Ala Glu Asp Ser Gly Val Tyr Tyr Cys Thr Asp
115 120 125

Phe Ile Asp Trp Gly Gln Gly Thr Leu
130 135

<210> 51

<211> 145

<212> PRT

<213> Mus musculus

<400> 51

Ala Leu Gln Leu Leu Ser Thr Gln Asp Leu Thr Met Arg Phe Ser Val
1 5 10 15

Gln Phe Leu Gly Val Leu Met Phe Trp Ile Ser Gly Val Ser Gly Asp

20

25

30

Ile Val Ile Thr Gln Asp Glu Leu Ser Asn Pro Val Thr Ser Gly Glu
35 40 45

Ser Val Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Tyr Lys Asp
50 55 60

Gly Lys Thr Tyr Leu Asn Trp Phe Leu Gln Arg Pro Gly Gln Ser Pro
65 70 75 80

Gln Leu Leu Met Tyr Leu Met Ser Thr Arg Ala Ser Gly Val Ser Asp
85 90 95

Arg Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Glu Ile Ser
100 105 110

Arg Val Lys Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Leu Val
115 120 125

Glu Tyr Pro Phe Thr Phe Gly Ser Gly Thr Lys Leu Glu Ile Lys Arg
130 135 140

Thr
145

<210> 52
<211> 116
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Humanised anti-CD23 antibody light chain variable region

<400> 52

Asp Ile Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val Thr Pro Gly
1 5 10 15

Glu Pro Ala Ser Ile Ser Cys Arg Ser Ser Lys Ser Leu Leu Tyr Lys
20 25 30

Asp Gly Lys Thr Tyr Leu Asn Trp Tyr Leu Gln Lys Pro Gly Gln Ser
35 40 45

Pro Gln Leu Leu Ile Tyr Leu Met Ser Thr Arg Ala Ser Gly Val Pro
50 55 60

Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile
65 70 75 80

Ser Arg Val Glu Ala Glu Asp Val Gly Val Tyr Tyr Cys Gln Gln Leu
85 90 95

Val Glu Tyr Pro Phe Thr Phe Gly Gln Gly Thr Lys Val Glu Ile Lys
100 105 110

Arg Thr Val Ala
115

<210> 53
<211> 444
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Humanised anti-CD23 antibody heavy chain variable region

<400> 53

Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly
1 5 10 15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Gly Tyr
20 25 30

Trp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
35 40 45

Ala Glu Ile Arg Leu Lys Ser Asp Asn Tyr Ala Thr His Tyr Ala Glu
50 55 60

Ser Val Lys Gly Lys Phe Thr Ile Ser Arg Asp Asp Ser Lys Ser Arg
65 70 75 80

Leu Tyr Leu Gln Met Asn Ser Leu Lys Thr Glu Asp Thr Ala Val Tyr
85 90 95

Tyr Cys Thr Asp Phe Ile Asp Trp Gly Gln Gly Thr Leu Val Thr Val
100 105 110

Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu Ala Pro Ser
115 120 125

Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys Leu Val Lys
130 135 140

Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser Gly Ala Leu
145 150 155 160

Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser Ser Gly Leu
165 170 175

Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser Leu Gly Thr
180 185 190

Gln Thr Tyr Ile Cys Asn Val Asn His Lys Pro Ser Asn Thr Lys Val
195 200 205

Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His Thr Cys Pro
210 215 220

Pro Cys Pro Ala Pro Glu Leu Ala Gly Ala Pro Ser Val Phe Leu Phe
225 230 235 240

Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val
245 250 255

Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe
260 265 270

Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro
275 280 285

Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr
290 295 300

Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val
305 310 315 320

Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala
325 330 335

Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg
340 345 350

Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly
355 360 365

Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro
370 375 380

Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser
385 390 395 400

Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln
405 410 415

Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn His
420 425 430

Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys
435 440